D0121 NP

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Figure 1A

```
  1   CGTCCGGCGGGGCGCAGGGCTGAGCGAGCGTCCGGGCTCCGGGGCTCCGGGGAAGGCGGT   60


 61   TGCAGCTCCTGAGTGCAGCGCGGCTTCCTGCCACTGTCCCGGCCCGGCCACCTCTCTGTC   120


121   ATGGCTCTGGCGGACAGCACACGTGGATTACCCAACGGGGGCGGCGGCGGGGGCGGCAGT   180
  1   M  A  L  A  D  S  T  R  G  L  P  N  G  G  G  G  G  G  S       20


181   GGCTCCTCGTCGTCCTCCGCGGAGCCACCGCTCTTCCCCGACATCGTGGAGCTGAACGTG   240
 21   G  S  S  S  S  A  E  P  P  L  F  P  D  I  V  E  L  N  V       40


241   GGGGGCCAGGTGTACGTGACCCGGCGCTGCACGGTGGTGTCGGTGCCCGACTCGCTGCTC   300
 41   G  G  Q  V  Y  V  T  R  R  C  T  V  V  S  V  P  D  S  L  L    60


301   TGGCGCATGTTCACGCAGCAGCAGCCGCAGGAGCTGGCCCGGGACAGCAAAGGCCGCTTC   360
 61   W  R  M  F  T  Q  Q  Q  P  Q  E  L  A  R  D  S  K  G  R  F    80


361   TTTCTGGACCGGGACGGCTTCCTCTTCCGCTACATCCTGGATTACCTGCGGGACTTGCAG   420
 81   F  L  D  R  D  G  F  L  F  R  Y  I  L  D  Y  L  R  D  L  Q    100


421   CTCGTGCTGCCCGACTACTTCCCCGAGCGCAGCCGGCTGCAGCGCGAGGCCGAGTACTTC   480
101   L  V  L  P  D  Y  F  P  E  R  S  R  L  Q  R  E  A  E  Y  F    120


481   GAGCTGCCAGAGCTCGTGCGCCGCCTCGGGGCGCCCCAGCAGCCCGGCCCGGGGCCGCCG   540
121   E  L  P  E  L  V  R  R  L  G  A  P  Q  Q  P  G  P  G  P  P    140


541   CCCTCGCGGCGCGGGGTGCACAAGGAGGGCTCGCTGGGTGACGAGCTGCTGCCGCTTGGC   600
141   P  S  R  R  G  V  H  K  E  G  S  L  G  D  E  L  L  P  L  G    160


601   TACTCGGAGCCCGAACAGCAGGAGGGCGCCTCTGCCGGGGCGCCGTCGCCCACGCTGGAG   660
161   Y  S  E  P  E  Q  Q  E  G  A  S  A  G  A  P  S  P  T  L  E    180


661   CTGGCTAGCCGCAGTCCGTCCGGGGGCGCGGCGGGCCCGCTGCTCACGCCGTCCCAGTCG   720
181   L  A  S  R  S  P  S  G  G  A  A  G  P  L  L  T  P  S  Q  S    200


721   CTGGACGGCAGCCGGCGCTCGGGCTACATCACCATCGGCTACCGCGGCTCCTACACCATC   780
201   L  D  G  S  R  R  S  G  Y  I  T  I  G  Y  R  G  S  Y  T  I    220


781   GGGCGGGACGCGCAGGCGGACGCCAAGTTCCGGCGAGTGGCGCGCATCACCGTTTGCGGA   840
221   G  R  D  A  Q  A  D  A  K  F  R  R  V  A  R  I  T  V  C  G    240


841   AAGACGTCGCTGGCCAAGGAGGTGTTTGGGGACACCCTGAACGAAAGCCGGGACCCCGAC   900
241   K  T  S  L  A  K  E  V  F  G  D  T  L  N  E  S  R  D  P  D    260
```

Figure 1B

```
 901  CGTCCCCCGGAGCGCTACACCTCGCGCTATTACCTCAAGTTCAACTTCCTGGAGCAGGCC   960
 261   R   P   P   E   R   Y   T   S   R   Y   Y   L   K   F   N   F   L   E   Q   A    280


 961  TTCGACAAGCTGTCCGAGTCGGGCTTCCACATGGTGGCGTGCAGCTCCACGGGCACCTGC  1020
 281   F   D   K   L   S   E   S   G   F   H   M   V   A   C   S   S   T   G   T   C    300


1021  GCCTTTGCCAGCAGCACCGACCAGAGCGAGGACAAGATCTGGACCAGCTACACCGAGTAC  1080
 301   A   F   A   S   S   T   D   Q   S   E   D   K   I   W   T   S   Y   T   E   Y    320


1081  GTCTTCTGCAGGGAGTGAGCTCCCCAGACCCCCTCGCCACTCCAGCGCCCAGTCCTTCTC  1140
 321   V   F   C   R   E                                                              325


1141  CTGCCCGAGAGATGATTACAGAGCCTCTTGTCCCACCTTTGTCCCCTGGCTGCTGCCCTC  1200


1201  CCATTCTCCCCCTCCAGTAGTAGCTGGGTGAGACCTGTCCGCCCACCTTCCCTCCACTAC  1260


1261  AGAACCTGCAGCCGCAAATCCTCTGGGCTGCTTCGTCTTCTTTGGACCTCCTGAACCGAG  1320


1321  AGAACCCAGAGGAACCCCCACCCCACCCCCACCTACCACTCCATGCTTTCTCTACTCCCT  1380


1381  GCCTCAAACCACCCCTCCCCCAGATGGTACTTCAGTTTGGATCTATTGGGGGAGTGTGGC  1440


1441  CACAGACCGGGGGATGATTGAATTGTTCAGAACCTGATTGGACCGTGTCCAATGTGCGGA  1500


1501  AGATTTCCTTGAAATCTTCTCAAGCTCTTATGACTCACTGGGGGTTTAAGAGATCAGGAT  1560


1561  TGGTTCCACTGTCTGGGGTTAGTGTTTTACAAGGTCATTACACAGTCTTTTTGACCTCTT  1620


1621  TTGAAGGTAGAGTTTTAGAAGGCTGGATGGAAGATTCTGAGCCTGGAATTAGGACCCCAT  1680


1681  GGAGGCAGTCCTCAAACCACCCCTCCCCCAGATGGTACTTCAGTTTGGATCTATTGGGGG  1740


1741  AGTGTGGCCACAGACCGGGGGATGATTGAATTGTTCAGAACCTGATTGGACCGTGTCCAA  1800


1801  TGTGCGGAAGATTTCCTTGAAATCTTCTCAAGCTCTTATGACTCACTGGGGGTTTAAGAG  1860


1861  ATCAGGATTGGTTCCACTGTCTGGGGTTAGTGTTTTACAAGGTCATTACACAGTCTTTTT  1920


1921  GACCTCTTTTGAAGGTAGAGTTTTAGAAGGCTGGATGGAAGATTCTGAGCCTGGAATTAG  1980
```

Figure 1C

```
1981    GACCCCATGGAGGCAGTTCAGTAACTAAACTAATAAAGTTTTGAAAAGTTACACGTAAAA    2040

2041    AAAAAAAAAAAA    2052
```

Figure 2A

```
                        1                                                  50
K+betaM6         (1)  MALADSTRGLPNGGGGGGGSGSSSSSAEPPLFPDIVELNVGGQVYVTRRC
KCNMB1           (1)  ----------MVKKLVMAQKRGETRALCLGVTMVVCAVITYYILVTTVL
K+Hnov27         (1)  ----MSRPLITRSPASPLXNQGIPTPAQLTKSNAPVHIDVGGHMYTSSLA
K+Hnov28         (1)  --------------------MDNGDWGYMMTDPVTLNVGGHLYTTSLT
KIAA1317         (1)  --QQQKKGTMALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHS
CG10465          (1)  --------------MSESMSGDHKILLKGHSSQYLKLNVGGHLYYTTIG
CG10830          (1)  -------------------------MPEIIELNVGGVSYTTTLA
K+channel_tetra  (1)  ------------------------MTSVEDVITLNVGGTMYTTTRS

                        51                                                 100
K+betaM6        (51)  TVVSVPDSLLWRMFTQQ----QPQELARDSKGRFFLDRDGFLFRYILDYL
KCNMB1          (40)  PLYQKSVWTQESKCHLIETNIRDQEELKGKKVPQYPCLWVNVSAAGRWAV
K+Hnov27        (47)  TLTKYPESRIGRLFDGTEP-----IVLDSLKQHYFIDRDGQMFRYILNFL
K+Hnov28        (29)  TLTRYPDSMLGAMFGGDFP------TARDPQGNYFIDRDGPLFRYVLNFL
KIAA1317        (49)  TLISIPHSLLWKMFSPKR--DTANDLAKDSKGRFFIDRDGFLFRYILDYL
CG10465         (36)  TLTKNNDTMLSAMFSGR------MEVLTDSEGWILIDRCGNHFGIILNYL
CG10830         (20)  TLLQDKSTLLAELFGEG-----RDSLAKDSKGRYFLDRDGVLFRYILDFL
K+channel_tetra (23)  TLSKETDTLLANTASGSLSEDEQANVVTLPDGTLFVDRDGPLFAYVLHFL

                        101                                                150
K+betaM6        (97)  RDLQLVLPDYFPERSRLQREAEYFELPELVRRLGAPQQPGPGPPPSRRGV
KCNMB1          (90)  LYHTEDTRDQNQQCSYIPGSVDNYQTARADVEKVRAKFQEQQ--------
K+Hnov27        (92)  RTSKLLIPDDFKDYTLLYEEAKYFQLQPMLLEMERWKQDRET--------
K+Hnov28        (73)  RTSBLTLPLDFKEFDLLRKEADFYQIEPLIQCLNDPKPLYP---------
KIAA1317        (97)  RDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQS--P------
CG10465         (80)  RDGTVPLPETNKEIAELLAEAKYCLTELAISCERALYAHQEPKPICRIP
CG10830         (65)  RDKALHLPEGFRERQRLLREAEHFKLTAMLECIRSERDARP---------
K+channel_tetra (73)  RTDKLSLPEQFREVARLKDEADFYRLERFSTLLSNASSISP---------

                        151                                                200
K+betaM6       (147)  HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGAAGPLLT
KCNMB1         (132)  --------------------------------------------------
K+Hnov27       (134)  --------------------------------------------------
K+Hnov28       (114)  --------------------------------------------------
KIAA1317       (139)  -------DEFCHSDFEDASQ--------------------GSDTRICP
CG10465        (130)  LITSQKEEQLLLSVSLKPAVILVVQRQNN------------KYSYTSTS
CG10830        (106)  --------------------------P-----------------------
K+channel_tetra(114)  -------------------------------------------RPRTANG

                        201                                                250
K+betaM6       (197)  PSQSLDGSRRSGYITIGYRGSYTIGRDAQADAKFRRVARITVCGKTSLAK
KCNMB1         (132)  --------VFYCFSAPRGNETSVLFQRLYGPQALLFSLFWPIFLLTGGLL
K+Hnov27       (134)  ----------GRFSRPCECLVVRVAPDLGERITLSGDKSLIEEVFPEIG
K+Hnov28       (114)  ---------MDTFEEVVELSSTRKLSKYSNPVAVIITQLTITTKVHSLL
KIAA1317       (160)  PSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAK
CG10465        (167)  DDNLLKNIELFDKLSLRFNERILFIKDVIGPSEICCWSFYGHGKKVAEVC
CG10830        (107)  ----------GCITIGYRGSFQFGKDGLADVKFRKLSRILVCGRVAQCR
K+channel_tetra(121)  YNTITSGAETGGYITLGYRG---------------------------

                        251                                                300
K+betaM6       (247)  EVFGDTLNESRDPDRP-PERYTSRYYLKFNFLEQAFDKLSESGFHMVACS
KCNMB1         (174)  IIAMVKSNQYLSILAAQK------------------------
K+Hnov27       (173)  DVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQVLERLQ-QRGFEIVGSC
K+Hnov28       (154)  EGISNYFTKWNKHMMDTRDCQVSFTFGPCDYHQEVSLRVHLMEYITKQGF
KIAA1317       (210)  EVFGETLNESRDPDRA-PERYTSRFYLKFKHLERAFDMLSECGFHMVACN
CG10465        (217)  CLTSIVYATDRKHTKVEFPEARIYEETLQVLLYENRNAPDQELMQATSSAR
CG10830        (146)  EVFGDTLNESRDPDHGGTDRYTSRFFLKHCYIEQAFDNLHDHGYRMAGSC
K+channel_tetra(141)  --------------------------------------------------
```

Figure 2B

```
                     301                                                 350
      K+betaM6  (296) STGTCAFASST---DQSEDKIWTSYTEYVFCRE----------------
        KCNMB1  (192) ------------------------------------------------
      K+Hnov27  (222) GGGVDSSQFSEYVLRRELRRTPRVPSVIRIKQEPL-------------
      K+Hnov28  (204) TIRNTRVHHMSERANENTVEHNWTFCRLARKTDD--------------
      KIAA1317  (259) SSVTASFIN-----QYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGK
       CG10465  (267) VGSASGTSINQYTSDEEEERTGLARLRSNKRNNPS-------------
       CG10830  (196) GSGTAGSAAEPKPGVDTEENRWNHYNEFVFIRD---------------
K+channel_tetra  (141) ------------------------------------------------


                     351                                                 400
      K+betaM6  (326) ------------------------------------------------
        KCNMB1  (192) ------------------------------------------------
      K+Hnov27  (257) ------------------------------------------------
      K+Hnov28  (238) ------------------------------------------------
      KIAA1317  (304) GDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPI
       CG10465  (302) ------------------------------------------------
       CG10830  (229) ------------------------------------------------
K+channel_tetra  (141) ------------------------------------------------


                     401                                                 450
      K+betaM6  (326) ------------------------------------------------
        KCNMB1  (192) ------------------------------------------------
      K+Hnov27  (257) ------------------------------------------------
      K+Hnov28  (238) ------------------------------------------------
      KIAA1317  (354) KKGPVQLIQQSEMRRKSDLLRTLTSGSRESNMSSKKKAVKEKLSIEEELE
       CG10465  (302) ------------------------------------------------
       CG10830  (229) ------------------------------------------------
K+channel_tetra  (141) ------------------------------------------------


                     451                        482
      K+betaM6  (326) ------------------------------
        KCNMB1  (192) ------------------------------
      K+Hnov27  (257) ------------------------------
      K+Hnov28  (238) ------------------------------
      KIAA1317  (404) KCIQDFLKIKIPDRFPERKHPWQSELLRKYHL
       CG10465  (302) ------------------------------
       CG10830  (229) ------------------------------
K+channel_tetra  (141) ------------------------------
```

Figure 3
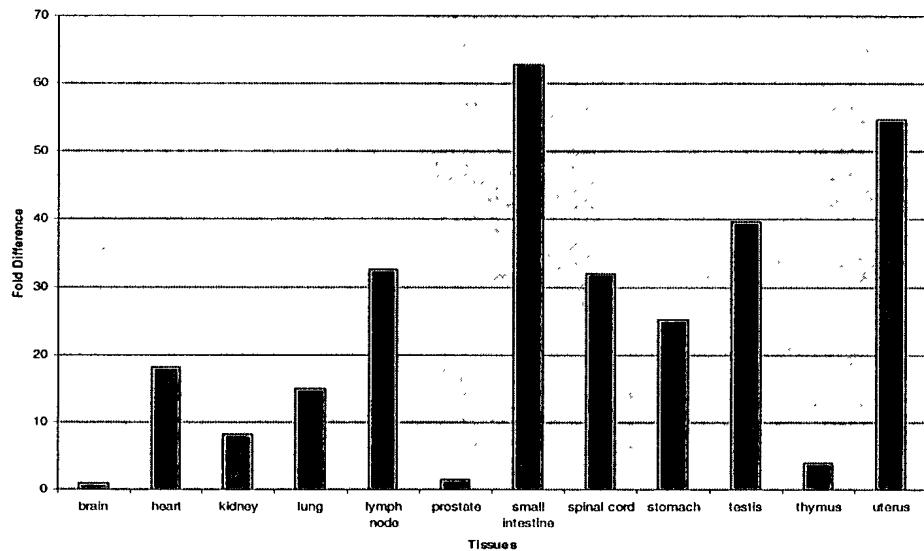
Figure 4.

Protein	Genbank / SWISS-PROT Accession No.	Identities	Similarities
human Maxi-K potassium channel beta subunit, KCNMB1 protein	gil4758625	0.0%	37.5%
human potassium channel K+Hnov27 protein	gilY34125	30.21%	39.15%
human potassium channel K+Hnov28 protein	gilY34129	30.04%	38.63%
Caenorhabditis elegans K+ channel tetramerisation domain containing protein	gil3880445	31.11%	39.26%
Drosophila CG10465 protein	gil17946205	23.9%	33.0%
Drosophila CG10830 protein	gil7300672	50.89%	62.5%
human KIAA1317 protein	gil7243015	60.42%	69.97%

D0121 NP

Figure 5